



PCT10

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/030,194

DATE: 11/18/2002  
TIME: 15:02:28

Input Set : A:\EP.txt  
Output Set: N:\CRF4\11182002\J030194.raw

```

7 <110> APPLICANT: RENARD, MICHEL
10      DELOURME, REGINE
13      BARRET, PIERRE
16      BRUNEL, DOMINIQUE
19      FROGER, NICOLE
22      TANGUY, XAVIER
28 <120> TITLE OF INVENTION: MUTANT GENE OF THE GRAS FAMILY AND PLANTS WITH REDUCED
29      DEVELOPMENT CONTAINING SAID MUTANT GENE
35 <130> FILE REFERENCE: 218874US0PCT
41 <140> CURRENT APPLICATION NUMBER: 10/030,194
44 <141> CURRENT FILING DATE: 2002-02-04
50 <150> PRIOR APPLICATION NUMBER: PCT/FR00/02216
53 <151> PRIOR FILING DATE: 2000-08-02
59 <150> PRIOR APPLICATION NUMBER: FR 9910023
62 <151> PRIOR FILING DATE: 1999-08-02
E--> 68 <160> NUMBER OF SEQ ID NOS: 63 see below
74 <170> SOFTWARE: PatentIn version 3.1

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## ERRORED SEQUENCES

Does Not Comply  
Corrected Diskette Needed

714 <210> SEQ ID NO: 3  
 717 <211> LENGTH: 1779  
 720 <212> TYPE: DNA  
 723 <213> ORGANISM: Brassica napus  
 729 <220> FEATURE:  
 732 <221> NAME/KEY: CDS  
 735 <222> LOCATION: (60)..(1778)  
 738 <223> OTHER INFORMATION:

*last sequence in submitted file*

*587 (see p.2)*

745 <400> 3	
747 caacccagaa caaaaaccaga ccgatctgag agattaacta tatcttaacc agatcagaa	59
751 atg aag agg gat ctt cat cag ttc caa ggt ccc aac cac ggg aca tca	107
753 Met Lys Arg Asp Leu His Gln Phe Gln Gly Pro Asn His Gly Thr Ser	
755 1 5 10 15	
759 atc gcc ggt tct tcc act tct tcc cct gcg gtg ttt ggt aaa gac aag	155
761 Ile Ala Gly Ser Ser Thr Ser Ser Pro Ala Val Phe Gly Lys Asp Lys	
763 20 25 30	
767 atg atg atg gtc aaa gaa gaa gac gac gag ctt cta gga gtc ttg	203
769 Met Met Met Val Lys Glu Glu Asp Asp Glu Leu Leu Gly Val Leu	
771 35 40 45	
775 ggt tac aag gtt agg tct tcg gag atg gct gag gtt gcg ttg aaa ctc	251
777 Gly Tyr Lys Val Arg Ser Ser Glu Met Ala Glu Val Ala Leu Lys Leu	
779 50 55 60	

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783 gag cag ctt gag acg atg atg ggt aac gct caa gaa gac ggt tta gct	299
785 Glu Gln Leu Glu Thr Met Met Gly Asn Ala Gln Glu Asp Gly Leu Ala	
787 65 70 75 80	
791 cac ctc gcg acg gat act gtt cat tac aac ccc gct gag ctt tac tcg	347
793 His Leu Ala Thr Asp Thr Val His Tyr Asn Pro Ala Glu Leu Tyr Ser	
795 85 90 95	
799 tgg ctt gat aac atg ctc acg gag ctt aac cca ccc gct gca acg acc	395
801 Trp Leu Asp Asn Met Leu Thr Glu Leu Asn Pro Pro Ala Ala Thr Thr	
803 100 105 110	
807 gga tct aac gct ttg aac ccg gag att aat aat aat aat aac tcg	443
809 Gly Ser Asn Ala Leu Asn Pro Glu Ile Asn Asn Asn Asn Asn Ser	
811 115 120 125	
815 ttt ttc acc gga ggc gac ctc aaa gcg att cct gga aac gcg gtt tgt	491
817 Phe Phe Thr Gly Gly Asp Leu Lys Ala Ile Pro Gly Asn Ala Val Cys	
819 130 135 140	
823 cgc aga tct aat cag ttc gcg ttt gcg gtt gat tcg tcg agt aat aag	539
825 Arg Arg Ser Asn Gln Phe Ala Phe Ala Val Asp Ser Ser Ser Asn Lys	
827 145 150 155 160	
831 cgt ttg aaa ccg tcc tcg agc cct gat tcg atg gtt aca tct cca tca	587
833 Arg Leu Lys Pro Ser Ser Pro Asp Ser Met Val Thr Ser Pro Ser	
E--> 835 165 170	195 ← insert

the  
correct  
nucleotide  
Total

**VERIFICATION SUMMARY**

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TIME: 15:02:29

Input Set : A:\EP.txt

Output Set: N:\CRF4\11182002\J030194.raw

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L:835 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:835 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1779 Found:587 SEQ:3  
L:68 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (6) Counted (3)